



Figure S3. Maximum-likelihood phylogenetic tree for concatenated MLST genes of *Wolbachia* isolates. The solid diamonds indicate the 2 strains identified from *Ae. aegypti* in this study. Where known, the names of the host species are given. The scale bar represents a 3% estimated difference in nucleotide sequence. Numbers given at each node correspond to the percentage bootstrap values (for 1,000 repetitions). Replicate numbers of <60% were not included in the figure. *Brugia malayi* *Wolbachia* ST-35 is used as an outgroup. Where available, the allelic profile for the assigned sequence type (ST) is provided in parentheses (gatB, coxA, hcpA, fbpA, ftsZ).